

FIGURE 1

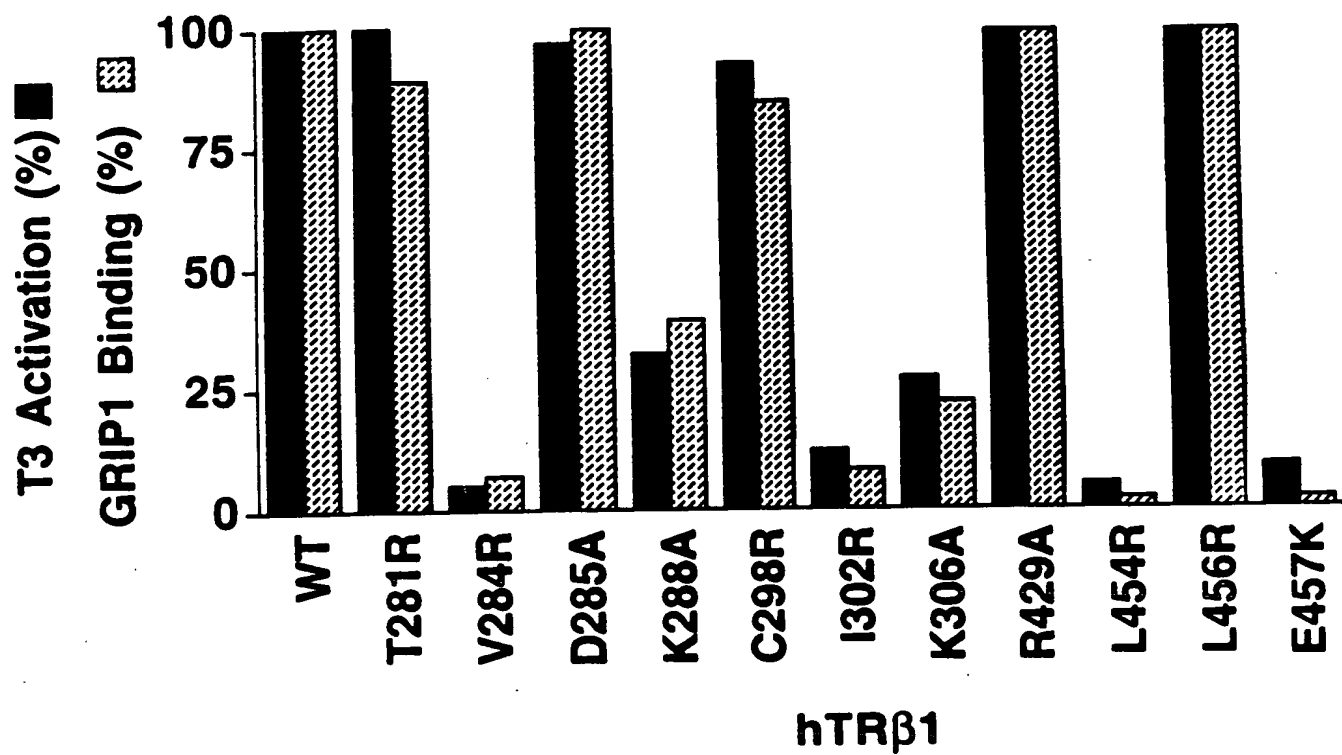


FIGURE 2

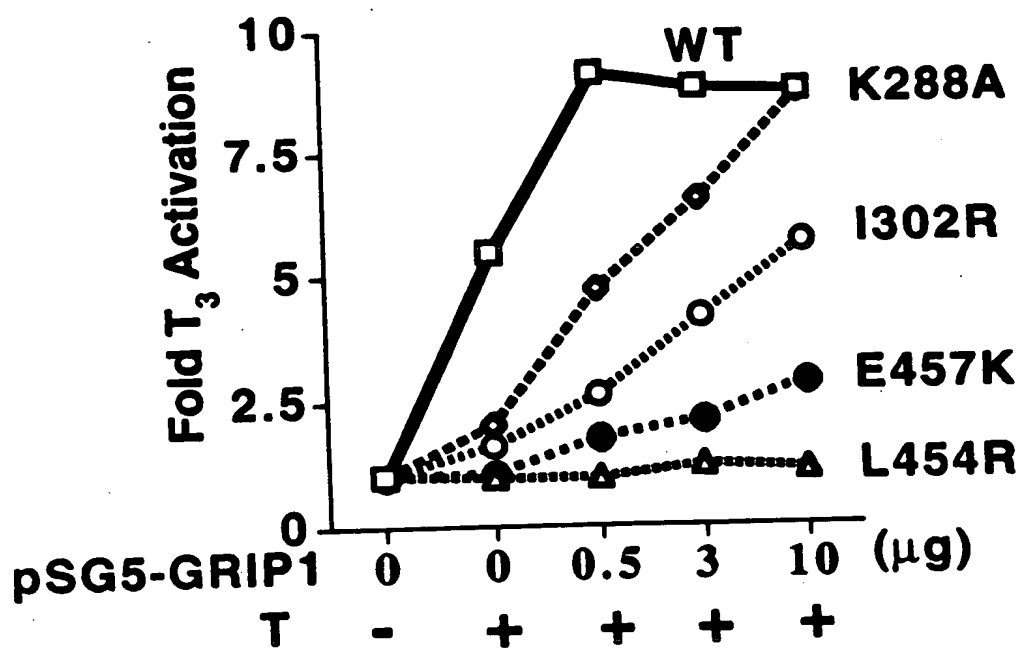


FIGURE 3

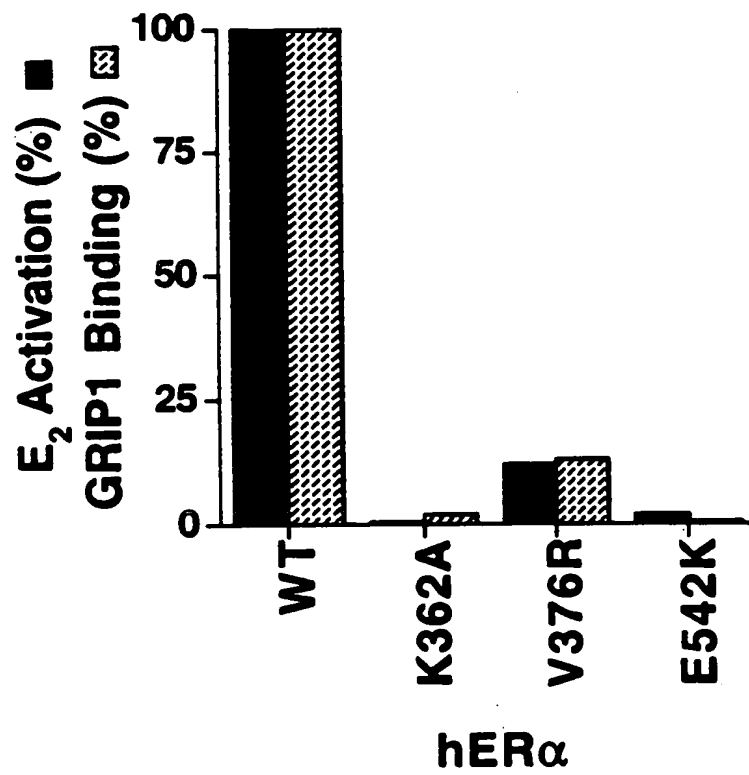
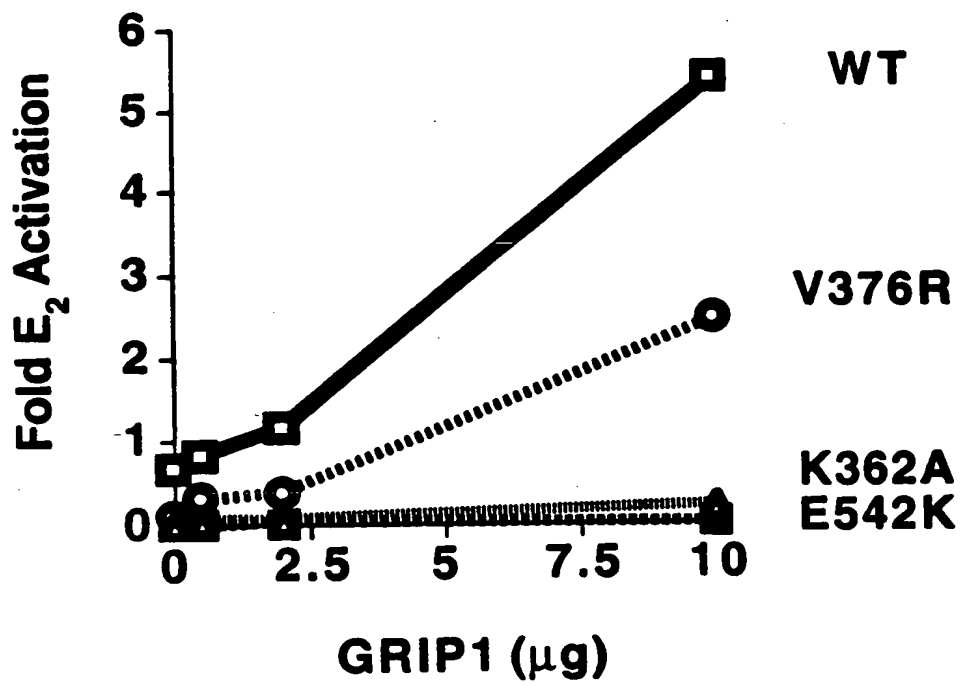


FIGURE 4



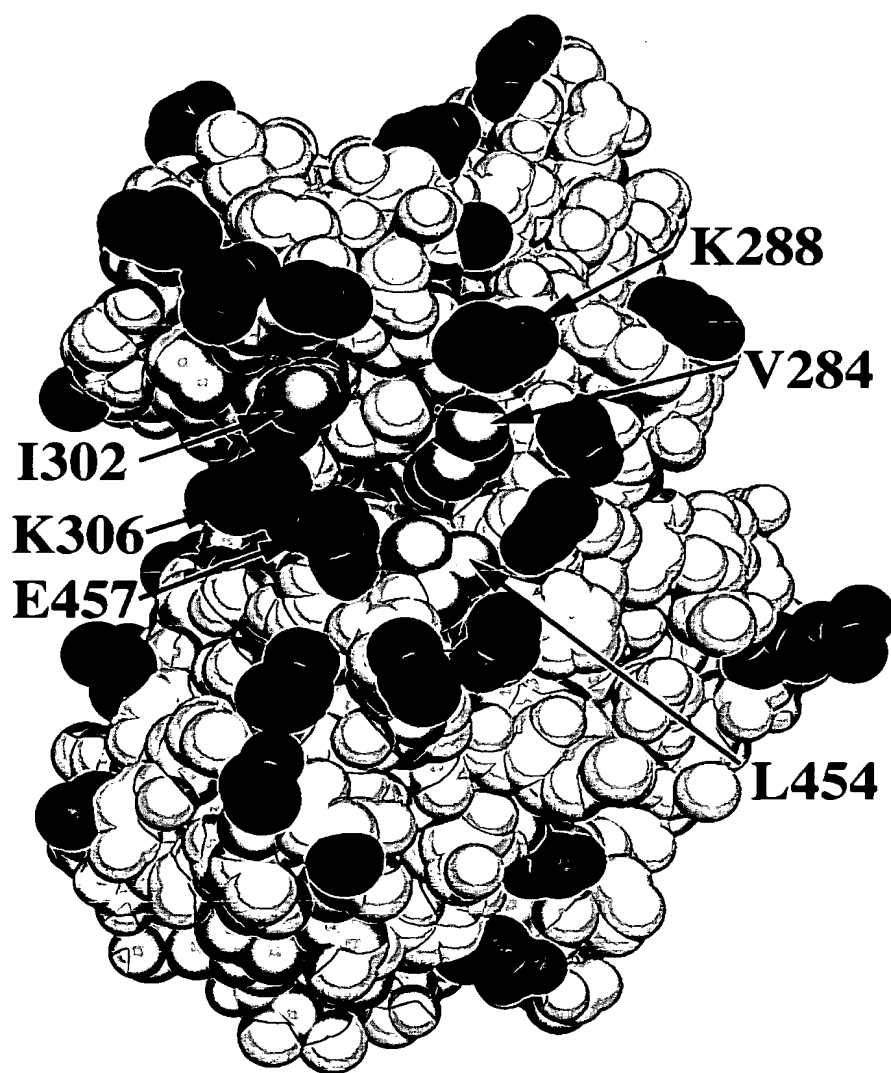


FIG 5

FIGURE 6






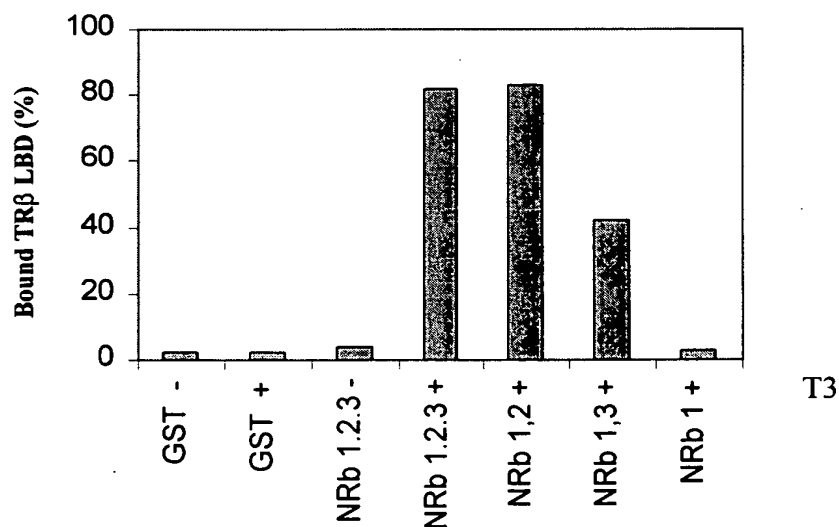
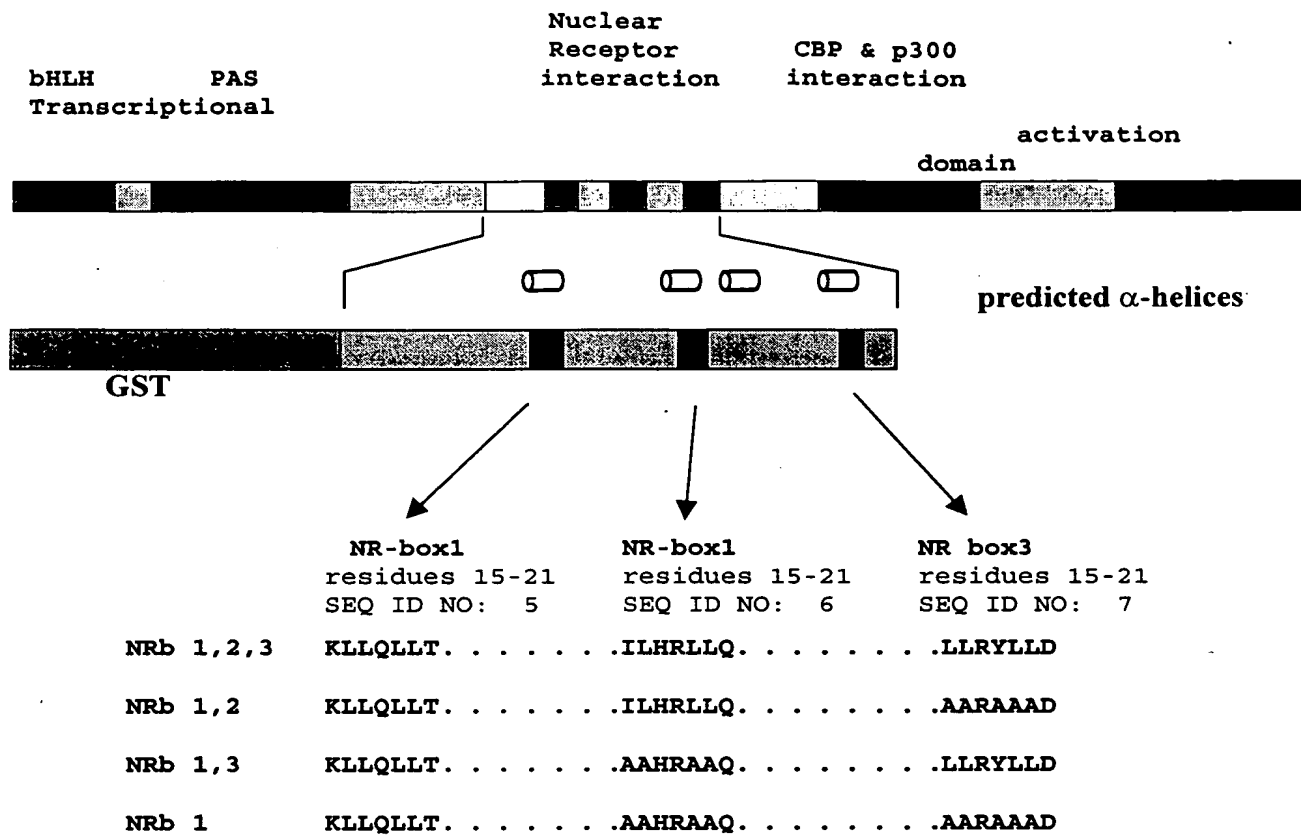
bHLH PAS Transcriptional		Nuclear Receptor interaction		CBP & p300 interaction	activation domain
					
					
	SEQ ID NO: 5	Grip1	AEGHSRLHDSKGQTKLLQLLTTKSEQMEPSPLAS		
	SEQ ID NO: 8	Tif2	ADGQSRLHDSKGQTKLLQLLTTKSEQMEPSPLAS		
	SEQ ID NO: 11	NcoA-2	AEGHSRLHDSKGQTKLLQLLTTKSEQMEPSPLPS		
	SEQ ID NO: 14	RAC3	AENQRGPLESKGHHKLLQLLTCSSDRGHSSLTN		
	SEQ ID NO: 17	AIB1, TRAM-1	AENQRGPLESKGHHKLLQLLTCSSDRGHSSLTN		
	SEQ ID NO: 20	p/CIP	SETPRGPLESKGHKLLQLLTCSSDRGHSSLTN		
	SEQ ID NO: 23	SRC1	SEGDSKY--SQTSHKLVQLLTTTAEQQLRHADID		
	SEQ ID NO: 26	Consensus	..-.....S....KLhQLLT...-.....		
	SEQ ID NO: 6	Grip1	PGSTHGTSLSKEKHKILHRLQLDSSSPVDLAKLTA		
	SEQ ID NO: 9	Tif2	SGSTHGTSLSKEKHKILHRLQLDSSSPVDLAKLTA		
	SEQ ID NO: 12	NcoA-2	PGSTHGTSLSKEKHKILHRLQLDSSSPVDLAKLTA		
	SEQ ID NO: 15	RAC3	TSNMHGSLLOEKHRILHKLLQNGNSPAEVAKITA		
	SEQ ID NO: 18	AIB1, TRAM-1	TSNMHGSLLOEKHRILHKLLQNGNSPAEVAKITA		
	SEQ ID NO: 21	p/CIP	TSNVHGSLLOEKHRILHKLLQNGNSPAEVAKITA		
	SEQ ID NO: 24	SRC1	TCPSSHSSSLTERHKILHRLQLG.GSPSDITTLVS		
	SEQ ID NO: 27	ConsensusL.E+H+ILH+LLQ...SP.-h..h..		
	SEQ ID NO: 7	Grip1	EPASPKKKE---NALLRYLLDKDDTKDIGLPEIT		
	SEQ ID NO: 10	Tif2	EPVSPKKKE---NALLRYLLDKDDTKDIGLPEIT		
	SEQ ID NO: 13	NcoA-2	EPASPKKKE---NALLRYLLDKDDTKDIGLPSIT		
	SEQ ID NO: 16	RAC3	EQLSPKKKE--NNALLRYLLDRDDPSDVLAKKLQ		
	SEQ ID NO: 19	AIB1, TRAM-1	EQLSPKKKE--NNALLRYLLDRDDPSDALSKELQ		
	SEQ ID NO: 22	p/CIP	EQLSPKKKE--NNALLRYLLDRDDPSDALSKELQ		
	SEQ ID NO: 25	SRC1	ELDAAKKKESKDHQLLRYLLDKDEKDLRSTPNLC		
	SEQ ID NO: 28	Consensus	E....KKKE.....LLRYLLD+D-.....h.		
Overall Consensus (SEQ ID NO: 1)		LXXLL.....		

FIGURE 7



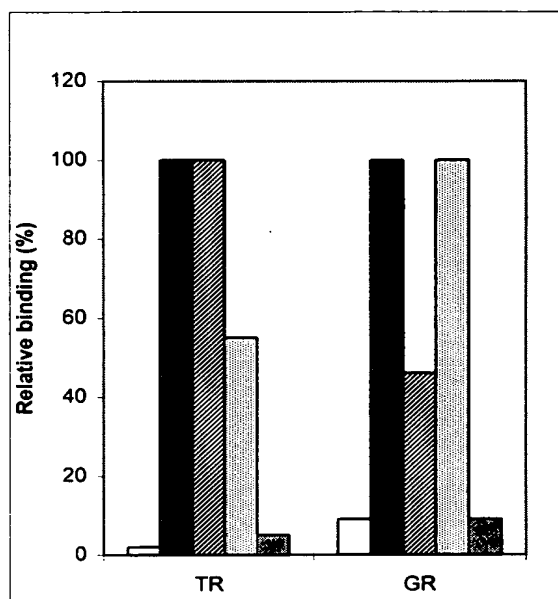
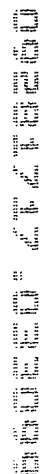


FIGURE 9

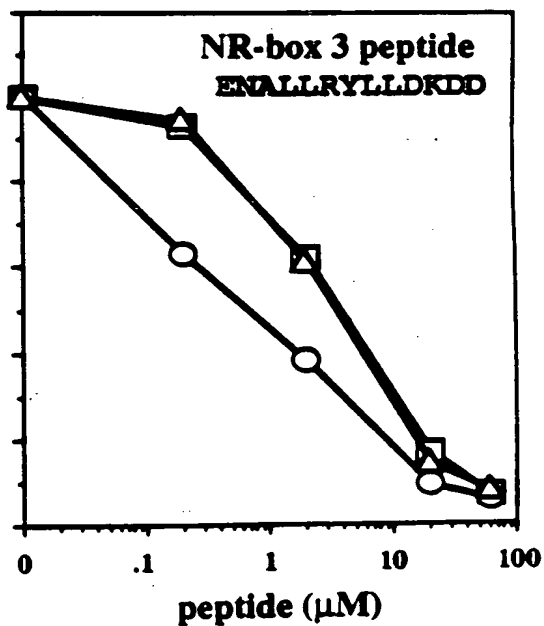
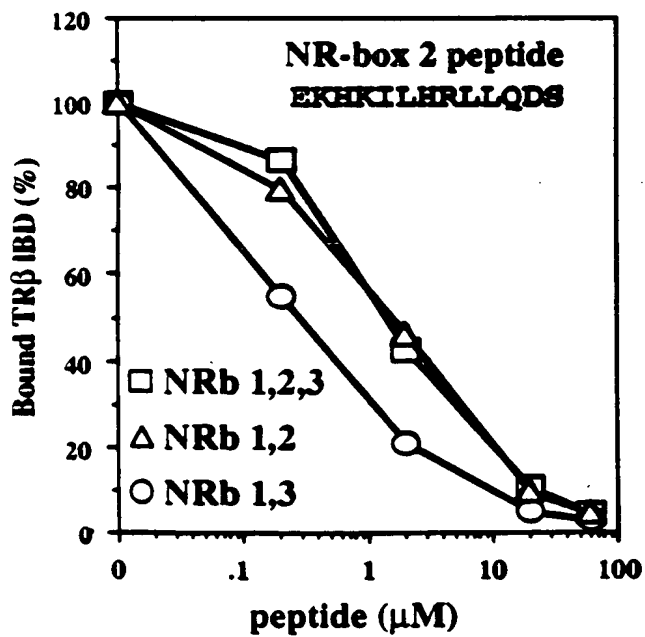
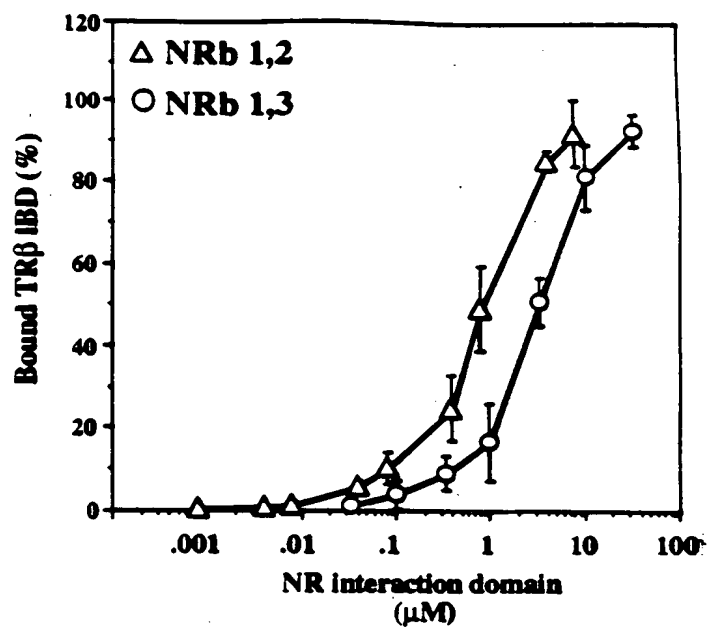


FIGURE 10

residues 11-23
residues 7-24
Of
SEQ ID NO: 6

●

▲

EKHK

TSLKEKHK

LLRYLL

LLRYLL

QDS

QDSS

■

●

▲

LLRYLL

LLRYLL

LLRYLL

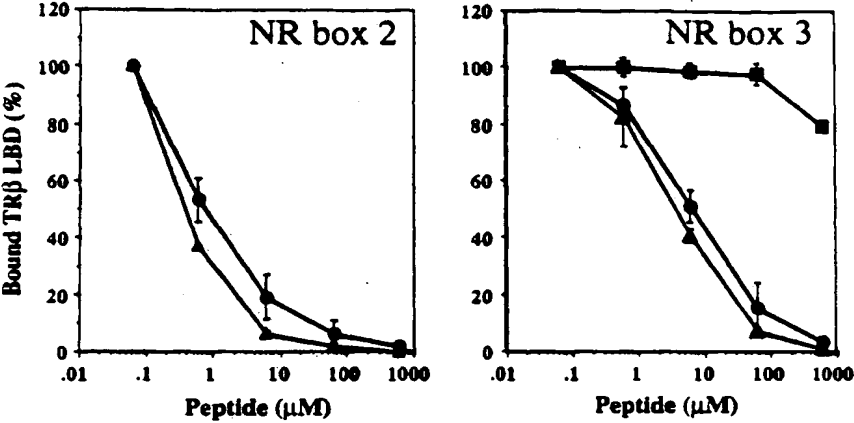
KENA

PKKKENA

DKDDTKD

DKDDTDK

residues 15-20
residues 11-27
residues 8-27
Of
SEQ ID NO: 7



residues 8027 of SEQ ID NO: 7
residues 11-27 of SEQ ID NO: 6
SEQ ID NO: 29

▲

▲

▲

PKKKENA

TSLKEKHK

TSLKEKHK

LLRYLL

LLRYLL

LLRYLL

DKDDTKD

QDSS

QDSS

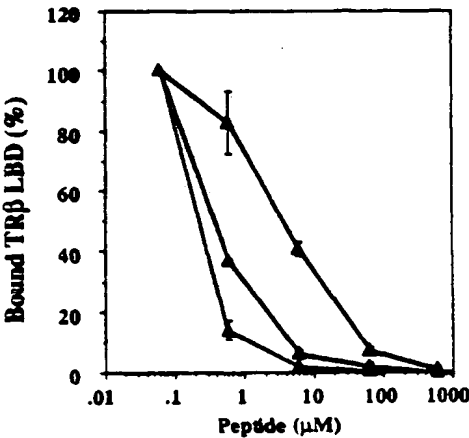


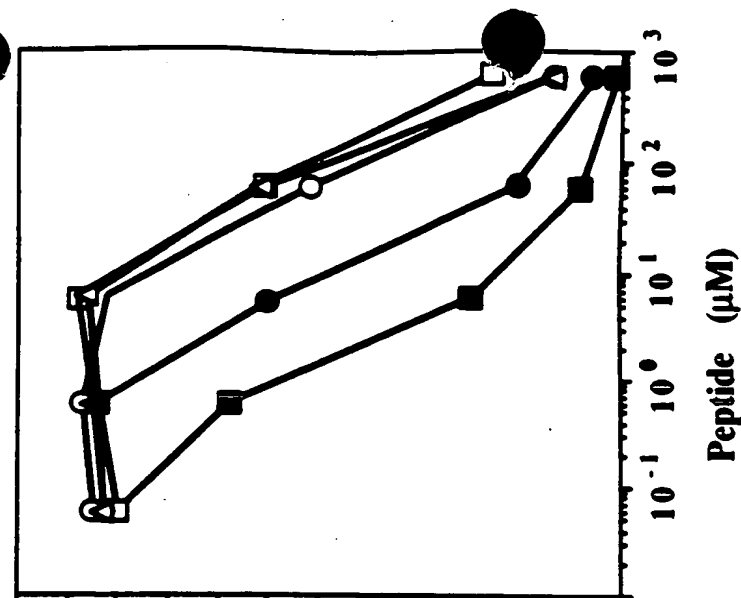
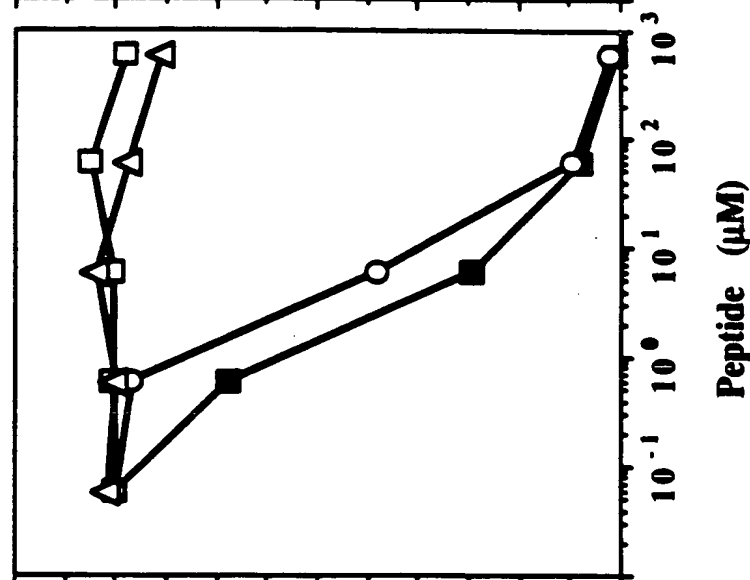
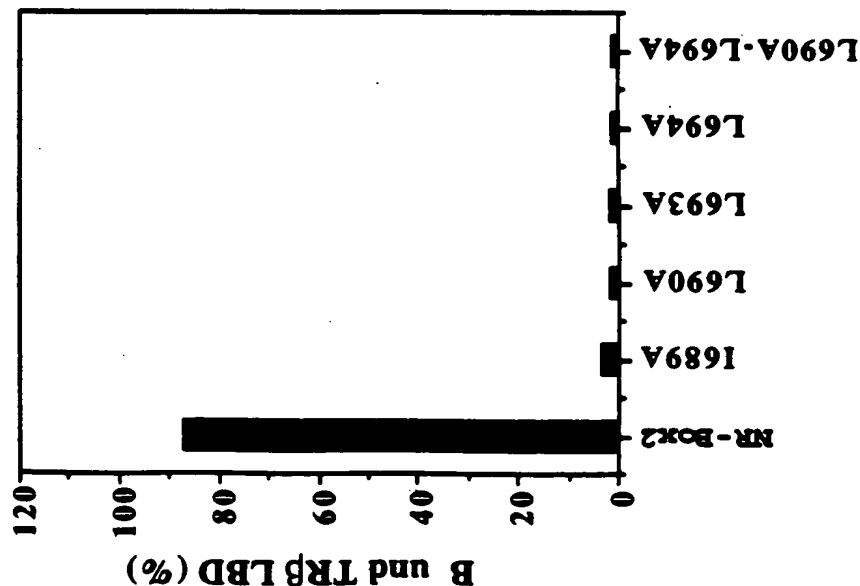
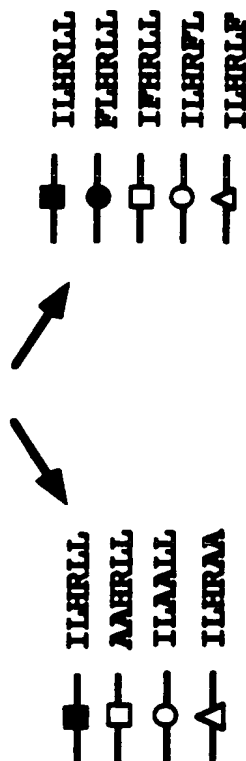
FIGURE 11

residues 12-24 SEQ ID NO: 6

NR-interaction
domain:

NRb 1,2
I689A
L690A
L693A
L694A
L690A/L694A
ILHRLL
ALHRLL
LAHRLL
ILHRAL
ILHRLA
LAHRLA

NR-box 2 peptide: KHK [ILHRLL] QDSS



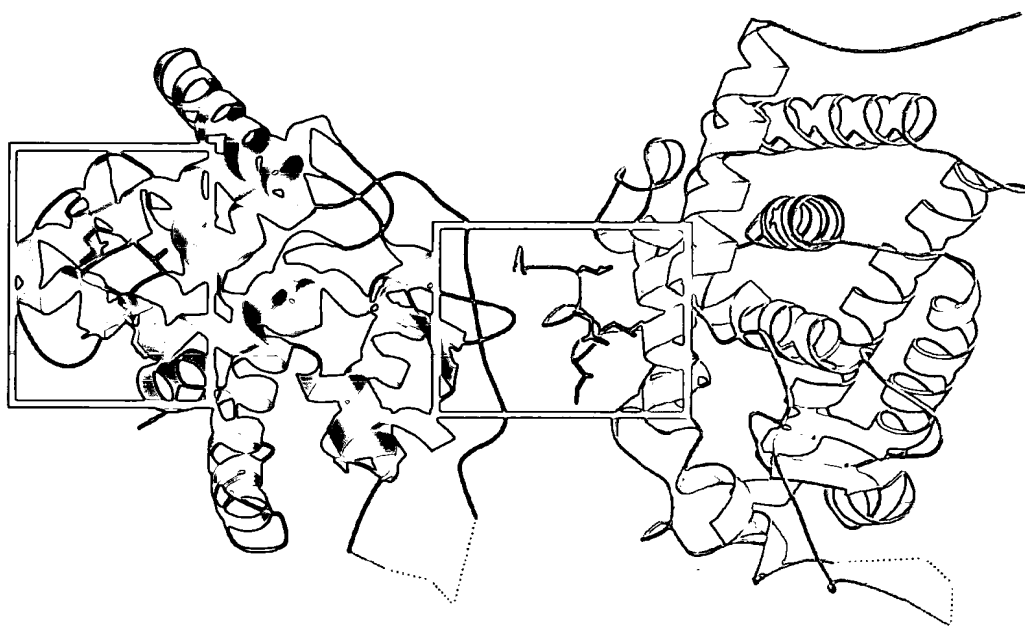


FIG 12

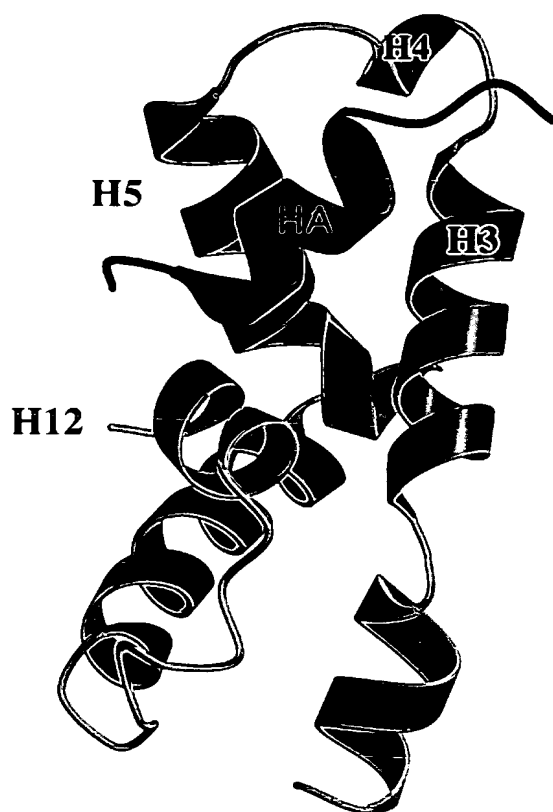


FIG. 13

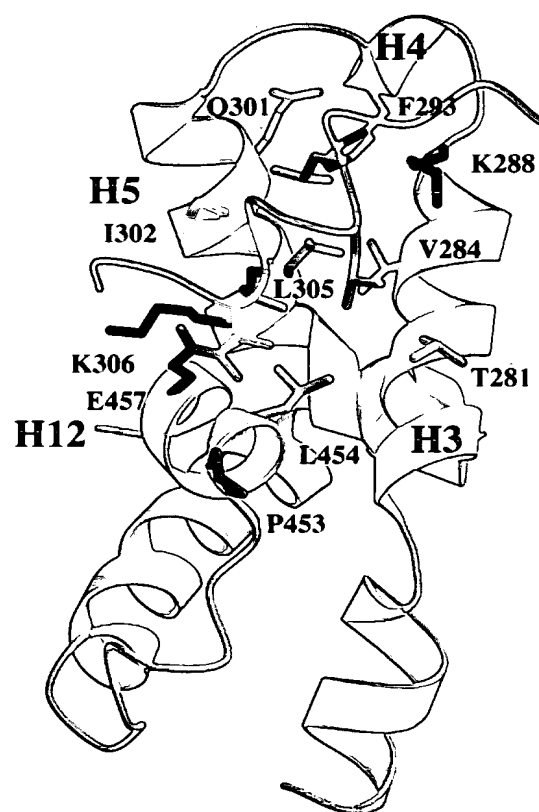


FIG. 14

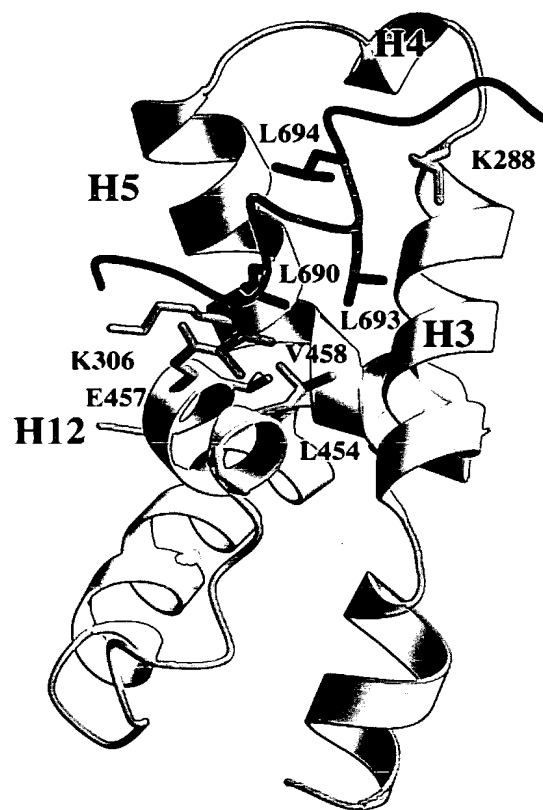


FIG 15

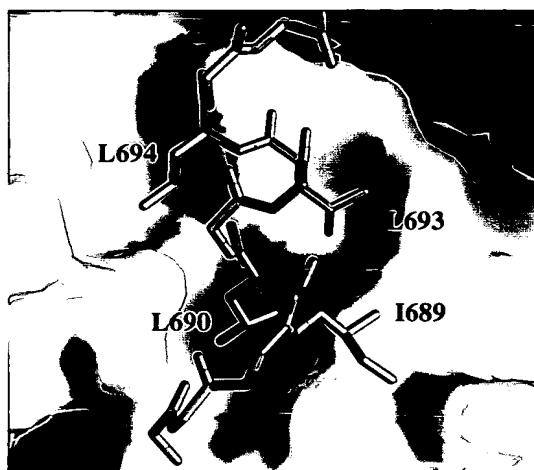


FIG 16

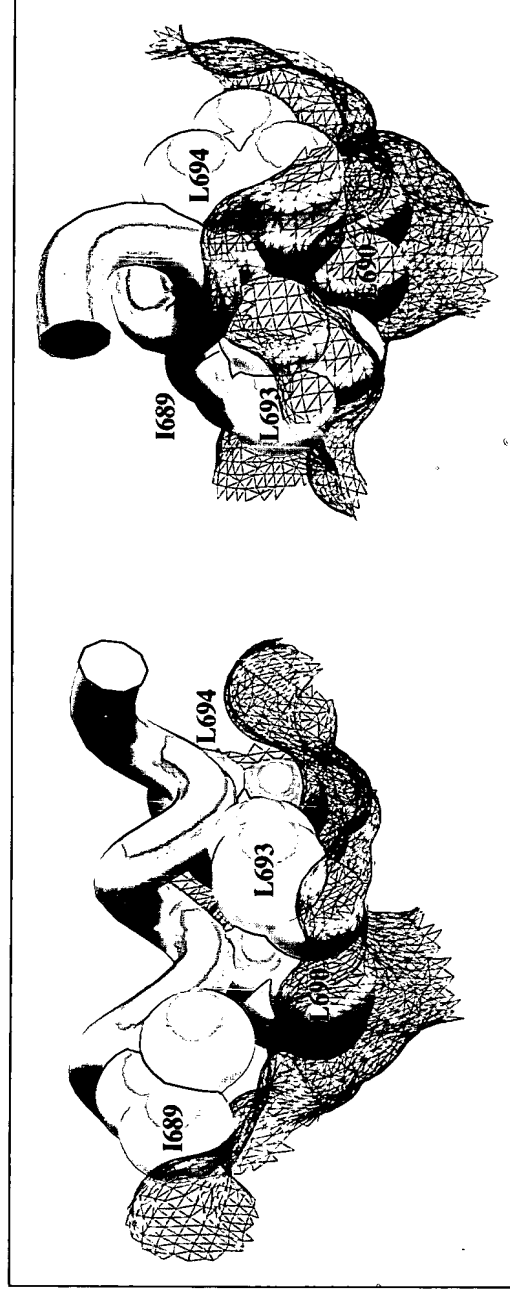


FIG. 17

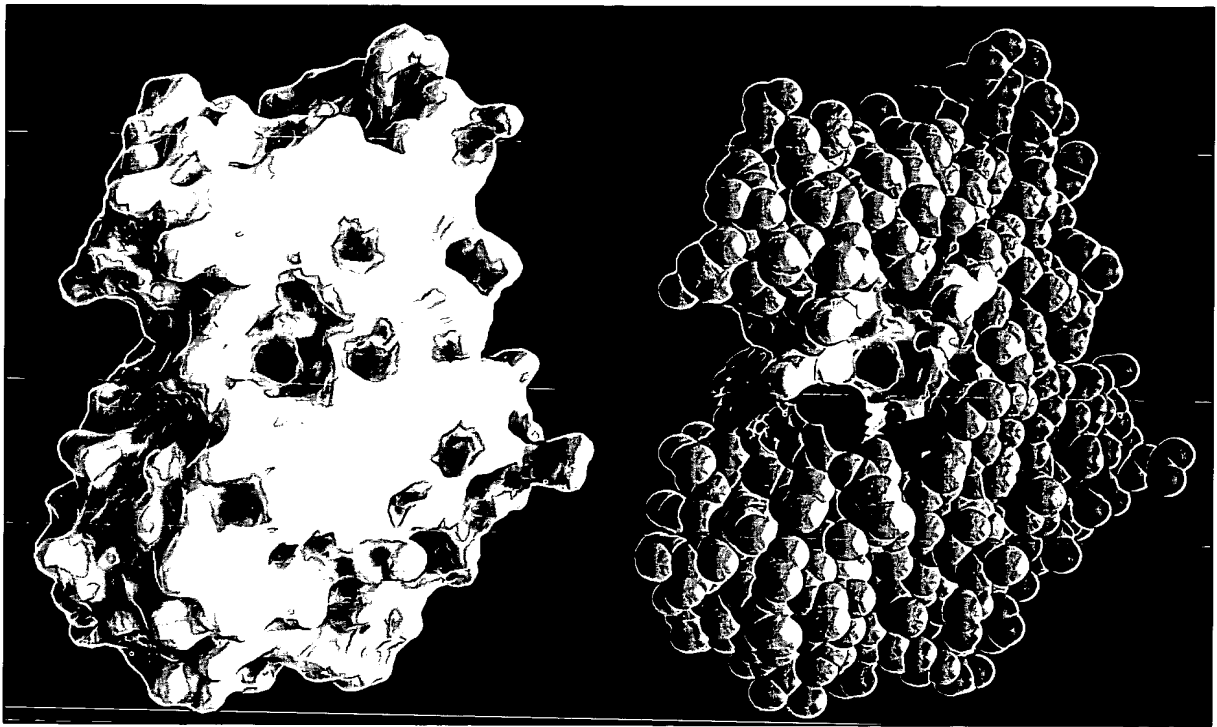


FIG 18

[illegible]

SBU	ID	NO:	31	b7cD
SBU	ID	NO:	33	c7cD
SBU	ID	NO:	35	b6AR
SBU	ID	NO:	37	b7cD
SBU	ID	NO:	39	b7AR
SBU	ID	NO:	41	Vvdr
SBU	ID	NO:	43	b7cD
SBU	ID	NO:	45	bDR
SBU	ID	NO:	47	bPR
SBU	ID	NO:	49	bMR
SBU	ID	NO:	51	bAR

FIGURE 19